CLAIMS

1. A method of producing a tumor host range (T-HR) mutant virus, wherein said T-HR mutant virus is unable to propagate in normal cells, but is able to propagate in abnormally proliferating cells, said method comprising the steps of:

(a) providing a wild-type viral DNA;

(b) introducing random mutations in said wild-type viral DNA, thereby obtaining a collection of uncharacterized mutant viruses;

(c) infecting abnormally proliferating cells with said collection of mutant viruses to amplify said mutant viruses;

(d) selecting mutant viruses that have the ability to proliferate in said abnormally proliferating cells from said collection by plaque isolation;

(e) infecting normally proliferating cells with mutant viruses selected in step (d);

(f) identifying mutant viruses from step (e) that do not proliferate in said normally proliferating cells, wherein said identified mutant virus are identified as a T-HR mutant viruses.

2. The method of claim 1, wherein said abnormally proliferating cell is uncharacterized.

3. The method of claim 1, wherein said virus has a mammalian host range.

4. The method of claim 3, wherein said mammal is a human.

5. The method of claim 1, wherein said virus is selected from the group consisting of simian virus 40 virus, human polyoma virus, parnovirus, papilloma virus, herpes virus, and primate adenoviruses.

6. The method of claim 1, wherein said T-HR mutant virus identified in step (f) infects a cell in which a tumor suppressor protein is not biologically active.

7. The method of claim 1, wherein said T-HR mutant virus identified in step (f) infects a cell in which an oncogene is expressed.

8. The method of claim 1, wherein said abnormally proliferating cell is a cancer cell.

9. The method of claim 1, wherein said viral DNA provided in step (a) is wild-type viral DNA.

10. The method of claim 1, wherein said collection of mutant viruses obtained in step (b) is uncharacterized.

11. A method of identifying a mammal having or at increased risk of acquiring a proliferative disease, said method comprising the step of determining whether there is a proliferative disease-associated alteration in a *Sal2* nucleic acid of said mammal.

12. The method of claim 11, wherein said method is for identifying a mammal having a proliferative disease.

13. The method of claim 11, wherein said method is for identifying a mammal at increased risk of acquiring a proliferative disease.

14. The method of claim 11, wherein said mammal is a human.

15. The method of claim 11, wherein said proliferative disease-associated alteration comprises the substitution of a Cys for the Ser at position 73 of SEQ ID NO:1.

16. The method of claim 11, wherein said determining is done by polymerase chain reaction (PCR) amplification, single nucleotide polymorphism (SNP) determination, restriction fragment length polymorphism (RFLP) analysis, hybridization analysis, or mismatch detection analysis.

17. The method of claim 11, wherein said method comprises the steps of:

(i) contacting a first nucleic acid probe which is specific for binding to said human *Sal2* nucleic acid containing said alteration with a nucleic acid from a cell from said mammal under conditions which allow said first nucleic acid probe to anneal to complementary sequences in said cell; and

(ii) detecting duplex formation between said first nucleic acid probe and said complementary sequences.

18. The method of claim 17, wherein said first nucleic acid probe is derived from the human *Sal2* nucleic acid containing a proliferative disease-associated alteration.

19. The method of claim 17, further comprising a second nucleic acid probe, wherein said first and second nucleic acid probes are PCR primers, and wherein said human *Sal2* nucleic acid or a fragment thereof is amplified using PCR between steps (i) and (ii).

20. The method of claim 17, wherein said cell is from a physiological sample containing abnormally proliferating tissue.

21. The method of claim 17, wherein said cell is from a physiological sample of normal tissue.

22. The method of claim 11, wherein said proliferative disease is cancer.

23. The method of claim 22, wherein said cancer is ovarian cancer.